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Corey Johnson

Signature January 18, 200

Date of Signature

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Scott et al.

Serial No.: 09/873,881

June 4, 2001 Filed:

For: Recombinant Multivalent Viral Vaccine

RESPONSE

Assistant Commissioner for Patents Box Sequence Washington, D.C. 20231

Sir:

1

In response to a Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, dated November 30, 2001, regarding sequence listing errors, Applicants herewith submit a corrected sequence listing as a Computer Readable Form and a Paper Copy. The CRF and the Paper Copy are the same. Applicants regret the error in the initial filing.

If any fee is due with this communication, please charge it to Deposit Account no. 08-2442.

Respectfully submitted,

HODGSON RUSS LLP

One M&T Plaza, Suite 2000 Buffalo, New York 14203-2391

(716) 848-1628

DATE: January 18, 2002

BFLODOCS: 648686 v1 (DWJ201!.DOC)









COMMISSIONER FOR PATENTS UNITED STATES PATENT AND TRADEMARK OFFICE

WASHINGTON, D.C. 20231 www.uspto.gov

APPLICATION NUMBER

FILING/RECEIPT DATE

FIRST NAMED APPLICANT

ATTORNEY DOCKET NUMBER

09/873,881

06/04/2001

Fred W. Scott

18617.NEW

CONFIRMATION NO. 6373

FORMALITIES LETTER

OC000000007141372*

Raniana Kadle Hodgson Russ LLP Suite 2000 One M&T Plaza Buffalo, NY 14203-2391

Date Mailed: 11/30/2001

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given TWO MONTHS FROM THE DATE OF THIS NOTICE within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

 A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

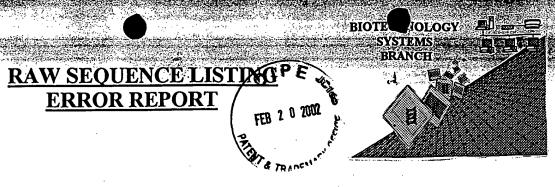
- For Rules Interpretation, call (703) 308-4216
- To Purchase Patentin Software, call (703) 306-2600
- For Patentin Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

A copy of this notice MUST be returned with the reply.

Customer Service Center

Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,88/ASource: $0/P \in 10/15/200/15$

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001 TIME: 15:47:14

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\1873881A.raw

- 3 <110> APPLICANT: Scott, Fred W.
- 5 <120> TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
- 7 <130> FILE REFERENCE: 18617.0016
- 9 <140> CURRENT APPLICATION NUMBER: US 09/873,881A
- 10 <141> CURRENT FILING DATE: 2001-06-04
- 12 <150> PRIOR APPLICATION NUMBER: US 08/552,369
- 13 <151> PRIOR FILING DATE: 1995-11-03
- 15 <160> NUMBER OF SEQ ID NOS: 19

Does Not Comply Corrected Diskette Needed

pg 1,3-4

ERRORED SEQUENCES

932	<210>	SEQ ID	NO: 19
933	<211>	LENGTH:	1979

- 934 <212> TYPE: DNA
- 935 <213> ORGANISM: feline leukemia virus
- 937 <220> FEATURE:
- 938 <223> OTHER INFORMATION:
- 940 <400> SEQUENCE: 19

941	acca	accaa	atc a	agad	cctct	to g	gacag	gece	ago	ctcag	gacg	atco	catca	aag		50
943	atg	gaa	agt	cca	acg	cac	cca	aaa	ccc	tct	aaa	gat	aag	act	ctc	95
944	Met	Glu	Ser	${\tt Pro}$	Thr	His	${\tt Pro}$	Lys	${\tt Pro}$	Ser	Lys	Asp	Lys	Thr	Leu	
945	1				5					10					15	
947	tcg	tgg	aac	tta	gcg	ttt	ctg	gtg	ggg	atc	tta	ttt	aca	ata	gac	140
948	Ser	Trp	Asn	Leu	Ala	Phe	Leu	Val	Gly	Ile	Leu	Phe	Thr	Ile	Asp	
949					20					25					30	
951	ata	gga	atg	gcc	aat	cct	agt	cca	cac	caa	ata	tat	aat	gta	act	185
952	Ile	Gly	Met	Ala	Asn	Pro	Ser	Pro	His	Gln	Ile	Tyr	Asn	Val	Thr	
953					35					40					45	
955	tgg	gta	ata	acc	aat	gta	caa	act	aac	acc	caa	gct	aac	gcc	acc	230
956	Trn	Va 1	Tle	Thr	Asn	Va1	Gln	Thr	Asn	Thr	Gln	Δla	Asn	Ala	Thr	

957 50 55 60 959 tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt 275 960 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val

960 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val 961 65 70 75

963 gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta 320 964 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu

965 85 90 967 aac cca acc aat gta aaa cac ggg gca cgt tac tcc tca aaa

968 Asn Pro Thr AsnUVal Lys His Gly Ala Arg Tyr Ser Ser Lys > 969 95 100 105

971 tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac 972 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr

972 TYP GIV CYS LYS THE THE ASP AIG LYS LYS GIR GIR GIR THE TYP

973

110

115

120

975 ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag

976 Dec Dec Dec Color Dec

976 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys 977 125 130 135 10 number are 455 in bold print Due to enor about - apostuple

365

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001 TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al
Output Set: N:\CRF3\10152001\1873881A.raw

980 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp 140 145 150 983 gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca 984 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser 985 155 160 165 987 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc 988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser W> 989 170 175 180 991 tgt gag gga aaa tgc acc ccc tg gtt ttg cag ttc acc cag aag 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys W> 993 185 190 195 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 997 999 cta tac cgt aca gga tat gac cct atc gct tta tc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser W> 1001 215 220 225 1003 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca acc 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1007 cta gtc tta cct gat caa aaa ccc cat cc ga caa tct caa aca 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr W> 1009 245 250 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala W> 1013 260 265 270 1019 acc gag gat gtt ata aat tta gta caa acg act gag acg att ggg 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Yr Leu Ala W> 1017 275 1019 acc gag gat ang gtt at aat att tta gta caa ggg act acg gac 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Yr Leu Ala W> 1021 290 295 1021 ctg gtt tct ca ca cac aca aca aca aca gad atg cac 1022 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Yr Leu Ala W> 1027 1029 1031 acc tac agc acc cca acc acc acc acc acc acc a		979	gga	aca	cat	tgt	gga	ggg	gca	caa	gat	ggg	ttt	tgt	gcc	gca	tgg	500
983 gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca 984 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser 985 155 160 165 987 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc 988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser W> 989 170 180 991 tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys 995 gga aga caa gcc tct tgg gac gga cct aag att ggg gga ttg cga 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 999 cta tac cgt aca gga tat gac cct atc ggt tt tc acc ggt gg 999 cta tac cgt aca gga tat gac cct cag gca atg ggg ccc aac 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser W> 1001 215 220 225 1003 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr W> 1009 245 250 255 1011 ggg tcc aaa gtg gg ga cc cag agg cc caa acg act gaa acg 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala W> 1013 260 265 270 1015 cca agg tct tgt gcc cc acc acc acg agg gcc caa acg gaa agg agg		980	Gly	Thr	His	Cys	Gly	Gly	Ala	Gln	Asp	Gly	Phe	Cys	Ala	Ala	Trp	
984 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser 155 160 165 987 tyg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc 988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser 170 175 180 991 tyt gag gga aaa tyc aac ccc ctg gtt ttg cag ttc acc cag aag 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys 995 gga aga caa gcc tct tyg gac gga cct aag aty tyg gga ttg cga 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 999 cta tac cgt aca gga at agac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 1003 cgg cag gta tca acc att acg cgc ct agg aat gga aga gga aga ca agac 1004 arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1004 arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1007 cta gtc tta cct gat caa aac cc tcc cgg caat tc caa aca 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr W> 1009 245 255 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala 1013 260 265 270 1015 cca agg tct gtt gcc ccc acc ac acg atg gga cca acg acg gat gga 260 285 1010 acg ga gat agg tta daa act act at att att gta caa ggg act ta cda gcc 1012 the Ash Ala Thr Asp Pro Ash Leu Val Gln Gly Thr Tyr Leu Ala 1024 Leu Ash Ala Thr Asp Pro Asn Leu Val Gln Gly Thr Tyr Leu Ala 1024 Leu Ash Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1024 Leu Ash Ala Thr Asp Pro Ash Leu Val Gln Gly Thr Tyr Leu Cys 1024 Leu Ash Ala Thr Asp Pro Ash Leu Val Gln Gly Thr Tyr Leu Cys 1025 1027 ctg gtt tct cga cca cc cat tac gaa ggg att gca atc tta gct 1024 Leu Ash Ala Thr Asp Pro Ash Leu Val Gln Gly Thr Tyr Leu Cys 1024 Leu Ash Ala Thr Asp Pro Ash Leu Val Gln Gly Thr Tyr Leu Cys 1025 1027 ctg gtt tct cga cca cc cac aca aca aca aca aca aca	W>	981					140					145					150	
155 160 165 590 165 987 tgg gac tat atc aca gta aaa aga gag agt agt cag gac aat agc gag agt are aga gag agt agt cag gac aat agc gag set agg gac aat agc gag gag tare aga gag aga tare aca gta aac cc ctg gtt ttg cag ttc acc aaa aga gag gag aga gag aga tare aga aga gag gag aga aga tare aga aga gag 202 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys gag ga aga caa gcc tct tgg gac gag cct aag agt ggg gat tg gag gag gag aga gag aga cac cct ttgg gac gag cct aag agt ggg gat tg gag gag gag 680 195 995 gga aga caa gcc tct tgg gac gag cct aag agt ggg ggt tg gag gag gag gag gag	1.	983	gga	tgt	gag	acc	acc	gga	gaa	gct	tgg	tgg	aag	CCC	acc	tcc	tca	545
987 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc 988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser 170 175 180 991 tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag 922 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys 995 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 1004 Arg Gln Val Ser Thr Pasp Cly Pro Lys Met Trp Gly Leu Arg 1004 Arg Gln Val Ser Thr Pasp Pro Ile Ala Leu Phe Thr Val Ser 1003 agg cag gta tca acc att acg ccg cct cag gca atg gga cca aac 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 230 235 240 1007 cta gtc tta cct gat caa aac cc cca cca acc acc 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr N-> 1009 245 250 255 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg acg caa tct caa acc 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala N-> 1013 260 265 270 1015 cca agg tct gtt gcc ccc acc acc acc atg ggt ccc aaa cgg act ggg 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly W> 1017 275 280 285 1012 Gly Ser Lys Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly W> 1019 acc gag gat agg tta ata aat tta gta caa gga aca tac ca gcc 201020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala W> 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala W> 1021 290 295 300 285 1024 1029 325 300 315 315 310 310 310 31 acc tac agc acc acc acc acc acc	11/	984	Gly	Cys	Glu	Thr	Thr	Gly	Glu	Thr	Trp	Trp	Lys	Pro	Thr	Ser	Ser	
988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser W> 989 170 175 180 180 199 991 tyt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys 995 gga aga caa gcc tct tyg gac gga cct aag aty tyg gga ttg cga 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 1000 4 rg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1004 arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1004 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr W> 1007 cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr W> 1013 260 265 270 1015 ca agg tct gtt gcc cc acc acc atg ggt ccc aaa agg aag gg 1016 Pro Arg Ser Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala W> 1017 275 280 285 1019 acc gga gat agg tta ata aat tta gta caa ggg aca cac gg att gg 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala W> 1021 290 295 300 905 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1031 acc tac aga cac caa aca aca ccc ccc ccc acc a	w¥>	985					155					160					165	
W-→ 989 170 175 180 991 tgt gag gag aaa tgc aac ccc tg gtt ttg cag ttc acc cag aag 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys W-→ 993 185 190 195 995 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg W-→ 997 200 205 210 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser W-→ 1001 215 220 225 1003 cgg cag gta tca acc att acg cct cag gca atg gga cca aac 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1007 cta gtc tta cca aaa acc cca tcc cga caa act caa caa 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr W-→ 1009 245 250 1011 ggg tcc aaa gtg gag acc caa agg acc aaa agg acc gac 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala W-→ 1013 260 265 1015 cca agg tct gtt gcc cca acc acc atc ggt ccaaa acg att ggg 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly W-→ 1017 275 1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala W-→ 1021 290 290 1023 tta aat gcc acc gac ccc acc acc aca aca ggg act gtg ct tgc 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1025 1027 ctg gtt tct cga cca ccc tat tac gaa ggg act gta tta gg 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1025 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta gt 1029 320 325 330 1031 acc tac agc aac caa aca aca acc ccc ccc cca tcc tgc cta tct act 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile 1033 ccg caa cac aaa caa aca acc cac cac gg tat ccg aca gga atg 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met 1037 350 355 360 1039 tgc ata ggg act gtt cct aaa cac acc aca gg ttt gc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys 1031 tac acc acc acc acc acc acc acc acc acc	\mathcal{N}	987	tgg	gac.	tat	atc	aca	gta	aaa	aga	ggg	agt	agt	cag	gac	aat	agc	590
991 tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys 993 185 190 195 995 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg N> 997 200 205 210 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser N> 1001 215 220 225 1003 cgg cag gta tca acc att acg cct ccag gca atg gga cca aac 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 210 235 240 1007 cta gtc tta cct gat caa aaa ccc cca tcc cga caat ct caa aca 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr N> 1009 245 250 255 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala N> 1013 260 265 270 1015 cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg 905 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly N> 1017 275 280 285 1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 950 1024 Leu Asn Ala Thr Asp Pro Asn Leu Val Gln Gly Thr Tyr Leu Ala N> 1021 290 295 300 295 300 1023 tta aat gcc acc gac ccc aac aaa acc aaa acc acc		988	Trp	Asp	Tyr	Ile	Thr	Val	Lys	Arg	Gly	Ser	Ser	Gln	Asp	Asn	Ser	
992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys 993 185 190 195 195 196 395 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga 680 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 200 205 210 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 1003 cgg cag gta tca acc att acg cgc cct cag gca atg gga cca acc 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1007 cta gtc tta cct gat caa aca acc cc atc cga caa tct caa aca 1007 cta gtc tta cct gat caa aca acc ccat tcc gga caa tct caa aca 1007 cta gtc tta cct gat caa aca ccc cca tcc cga caa tct caa aca 1001 ggg tcc aaa gtg gcg acc cag agg ccc caa acg act caa aca 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg act gaa agc gcc 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg act gaa agc gcc 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala 1015 cca agg tct gtt gcc ccc acc acc acg ggt ccc aaa cgg att ggg 905 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly 1017 275 280 285 1019 acc gga gat agg tta ata act tta gta caa ggg aca tac cta gcc 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala 1021 290 290 295 300 1023 tta act gcc acc gcc ccc acc acc acc acc acc acc	W>	989	_	_			170					175					180	
W-→ 993		991	tgt	gag	gga	aaa	tgc	aac	ccc	ctg	gtt	ttg	cag	ttc	acc	cag	aag	635
995 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg W> 997		992	Cys	Glu	Gly	Lys	Cys	Asn	Pro	Leu	Val	Leu	Gln	Phe	Thr	Gln	Lys	
996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 205 210 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 220 225 240 225 240 200 245 250 255	W>	993	_				185					190					195	
W> 997		995	gga	aga	caa	gcc	tct	tgg	gac	gga	cct	aag	atg	tgg	gga	ttg	cga	680
999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 1003 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca acc 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 1007 cta gtc tta cct gat caa aca ccc cca tcc cga caa tct ca aca aca 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala 1015 cca agg tct gtt gcc cca aca aca at ggg ccc aaa cgg att ggg 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly 1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala 1021 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala 1023 tta aat gcc acc gac ccc acc aca aca aca gac tgt tgg ctc tgc 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1031 acc tac aga acc cac ccc tat tac gaa ggg att gca atc tta ggt 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile 1035 ccg caa cac aca cac acc acc acc acc acc		996	Gly	Arg	Gln	Ala	Ser	Trp	Asp	Gly	Pro	Lys	Met	Trp	Gly	Leu	Arg	
1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 225 225 225 225 225 226 225 226 225 226 225 226 225 226 2	W>	997					200					205					210	
W> 1001		999	cta	tac	cgt	aca	gga	tat	gac	cct	atc	gct	tta	ttc	acg	gtg	tcc	725
1003 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac 770 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 230 230 235 240 1007 cta gtc tta cct gat caa aaa ccc cat cc cga caa tct caa aca 815 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr 255 1011 ggg tcc aaa gtg gcg acc caa agg ccc caa acg aat gaa agc gcc 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala 260 1015 cca agg tct gtt gcc ccc acc acc acg agg ccc aaa cgg att ggg 905 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly 275 1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 950 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala 290 1021 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 305 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 320 1025 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1031 acc tac agc acc caa aca acc ccc ccc ccc ccc c		1000	Leu	Tyr	Arg	Thr	Gly	туг	Asp	Pro	Ile	: Ala	Leu	Phe	Thr	· Val	Ser	
1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 230	W>																	
1007 cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca 815																		770
1007 cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca	4.	1004	Arg	Gln	val	Ser	Thr	Ile	Thr	Pro	Pro	Glr	Ala	Met	: Gly	Pro	Asn	
Note 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr 245 250 255 255 1011 ggg toc aaa gtg gcg acc cag agg ccc caa acg aat gaa agg gcc 860 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Ala Pro Thr Thr Met Gly Pro Lys Arg Tle Gly Gln	WF->,																	
W> 1009	10																	815
1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc 860 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala W> 1013 260 265 270 1015 cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg 905 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly W> 1017 275 280 285 1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 950 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala W> 1021 290 295 300 1023 tta aat gcc acc gac ccc aac aaa act aaa act aaa act tag gt tgg ct tgc 995 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 305 305 310 315 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040 1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 1029 320 325 330 1031 acc tac agc aac caa aca acc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Pro Ser Cys Leu Ser Ile W> 1033 335 340 345 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037 350 350 351 360 1039 tgc ata ggg act gtt cct aaa acc cac cac cag agc ttt gtgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365	λ	1008	Leu	Val	. Leu	Pro	Asp	Gln	Lys	Pro	Pro	Ser	Arg	Glr	Ser	Gln	Thr	
1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala 260 265 270	M>																	
W> 1013																		860
1015 cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg 905 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly W> 1017			_	Ser	Lys	Val			Gln	Arg	Pro			Asn	GIU	ı Ser		•
1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly N> 1017 275 280 285 2	M>																	
W> 1017																		905
1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 950 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala 290 295 300 1023 tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc 995 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 305 310 315 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040 1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 1029 320 325 330 1031 acc tac agc aac caa aca aca ccc ccc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile W> 1033 335 335 340 345 1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037 350 350 355 360 1039 tgc ata ggg act gtt cct aaa acc cac cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375				Arg	Ser	val			rnr	Thr	мет			гуу	Arg	Tre		
1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala W> 1021	M>																	050
W> 1021					-						-							950
1023 tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc 995 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 305 310 315 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040 1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 1029 320 325 330 1031 acc tac agc aac caa aca aca ccc ccc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile W> 1033 335 340 345 1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037 350 355 360 1039 tgc ata ggg act gtt cct aaa acc cac cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375				GTA	ASP	Arg			ASII	ьeu	. vaı		_	T 111T	. 1 Y 1	. Leu		
1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 1025	W>			+		200					20+			+ 4+	+ 00	, ata		005
N> 1025 305 310 315 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040 1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 1029 320 325 330 1031 acc tac agc aac caa aca aca ccc ccc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile N> 1033					-													223
1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040 1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 1029 320 325 330 1031 acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile W> 1033 335 340 345 1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037 350 355 360 1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375	A			MSII	. Ala	1111	_		, veii	цуз	1111			Cys	, 111	, nea		
1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 1029 320 325 330 1031 acc tac agc aac caa aca acc ccc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile W> 1033 335 345 1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037 350 355 360 1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375	7			att	tat	cas			tat	tac	таа			αca	ato	tta		1040
1029 320 325 330 1031 acc tac agc aac caa aca acc ccc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile W> 1033 335 345 1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037 350 355 360 1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 375	1/-	٠.	_	-		_					_			_				1010
1031 acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act 1085 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile W> 1033	يرا للا	/		, vai	Der	nrg			· -1-	7 -	Olu	-						
1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile W> 1033				tac	age	aac			aac	CCC	ccc			tac	e ota	t.ct.		1085
<pre>W> 1033</pre>	∕ / .				_													
1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037	W>			-1-	001									-1-				
1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met W> 1037 1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375	" "			caa	cac	aaa			ata	tet	σaa			gga	caa	qqa		1130
W> 1037 350 355 360 1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375																		
1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375	W>			O-11	0	-1-								1		1		
1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys W> 1041 365 370 375	** **			ata	gaa	act			aaa	acc	cac			tta	tac	aat		1175
W> 1041 365 370 375																		
	W>		_		1				4-						_			
				caa	cag	gga			ggg	gcg	cac			gcc	geo	ccc	aac	1220

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001 TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\1873881A.raw

			Gln	Glr	ı Gly			Gly	Ala	a His		Leu	Ala	Ala	Pro	Asn	
W>	1045					380					385					390	
	1047	ggc	acc	tat	: tgg	gcc	: tgt	aac	act	: gga	cto	acc	cca	tgc	att	tcc	1265
			Thr	туг	Trp			Asn	Thr	Gly		Thr	Pro	Cys	Ile	Ser	
W>	1049					395					400					405	
	1051	atg	gcg	gtg	cto	aat	. tgg	acc	tct	gat	ttt	. tgt	gtc	tta	atc	gaa	1310
			Ala	Val	. Leu			Thr	Ser	Asp	Phe	Cys	Val	Leu	Ile	Glu	
W>	1053					410					415					420	
	1055	tta	tgg	ccc	aga	gtg	act	. tac	cat	caa	ccc	gaa	tat	gtg	tac	aca	1355
			Trp	Pro	Arg			Tyr	His	Gln		Glu	Tyr	Val	Tyr	Thr	
W>	1057					425					430					435	
	1059	cat	ttt	gcc	aaa	gct	gtc	agg	ttc	cga	aga	gaa	cca	ata	tca	cta	1400
	1060		Phe	Ala	Lys			Arg	Phe	Arg			Pro	Ile	Ser	Leu	
M>	1061					440					445					450	
	1063	acg	gtt	gcc	ctt	atg	ttg	gga	gga	ctt	act	gta	ggg	ggc	ata	gcċ	1445
	1064	Thr	Val	Ala	Leu		Leu	Gly	Gly	Leu			Gly	Gly	Ile	Ala	
W>	1065					455					460					465	
	1067	gcg	ggg	gtc	gga	aca	ggg	act	aaa	gcc	ctc	ctt	gaa	aca	gcc	cag	1490
	1068	АТа	GLY	Val	GLY		GLy	Thr	Lys	Ala		Leu	Glu	Thr	Ala		
W>	1069				_4_	470					475					480	
	1071	LLC	aga	caa	Cta	caa	atg	gcc	atg	cac	aca	gac	atc	cag	gcc	cta	1535
T.T .	1072 1073	Pne	Arg	GIII	Leu		met	Ala	мет	HIS		Asp	He	GIn	Ala		
W>		~~~	~	+	-++	485					490					495	
	1075	Clu	gaa	Com	TIO	con	315	LLd	gaa	aag	tcc	ctg	acc	tcc	ctt	tct	1580
W>	1076 1077	GIU	GIU	ser.	TTE	500	нта	Leu	Giu	гуѕ		Leu	Thr	ser	ьeu		
W>	1077	maa	αt a	ata	tt a		220	3.63	~~~	~~~	505	~~+				510	1.605
	1080	Glu	Val	Val	T.OII	Cln	Acn	Ara	λra	2111	Tou	yaı	Tio	Cta	Dho	tta Tau	1625
W>	1081	GIU	val	Val	Leu	515	MSII	AIG	Ary	GIU	520	ASP	TTE	Leu	Pne		
**/		саа	αaα	ααa	aaa		tat	acc	aca	tta		~ ~ ~	~ ~ ~ ~	+ ~+.	+~~	525	1670
	1084	Gln	Glu	Glv	Glv	Len	Cvs	Δla	Δla	LLG	Tage	Glu	Clu	Cvc	Cvc	Dho.	10/0
W>	1085	· · · · ·	014	011	011	530	CID		mru	Deu	535	GIU	GIU	Cys	Cys	540	
••	1087	tat	aca	σat.	cac		σσα	ctc	atc	сда		aat	atα	acc	222		1715
	1088	Tyr	Ala	Asp	His	Thr	Glv	Leu	Val	Ara	Asp	Agn	Met	Δla	Lvs	T.eu	1/13
W>	1089	•		-		545	1			5	550				_, _	555	
	1091	aga	gaa	aqa	cta	aaa	caq	caa	caa	caa	cta	ttt	gac	tee	саа		1760
	1092	Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln	_,,,,
W>		_		_		560					565					570	
	1095	gga	tgg	ttt	gaa	gga	tgg	ttc	aac	aag	tcc	ccc	tqq	ttt	aca	acc	1805
	1096	Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr	
W>		•				575					580		-			585	
	1099	cta	att	tcc	tcc	att	atg	ggc	ccc	tta	cta	atc	cta	ctc	cta	att	1850
	1100	Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Leu	Ile	
M>						590 .					595					600	
	1103	ctc	ctc	ttc	ggc	cca	tgc	atc	ctt	aac	cga	tta	gta	caa	ttc	gta	1895
	1104	Leu	Leu	Phe			Cys	Ile	Leu	Asn	Arg	Leu	Val	Gln	Phe	Val	
M>						605					610					615	
	1107	aaa	gac	aga	ata	tct	gtg	gta	cag	gct	tta	att	tta	acc	caa	cag	1940
M>	1108	Lys	Asp/	Axg	Ile	Ser	Val	Val	${ t Gln}$	Ala	Leu	Ile	Leu	Thr	Gln	Gln	
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RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/873,881A

TIME: 15:47:15

1.979

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\1873881A.raw

620 630 W--> 1109 625

1111 tac caa cag ata aag caa tac gat ccg gac cga cca tga

1112 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro

635 W--> 1113

E--> 1117/bFLOdOcs:589477_1 (cm%d01)

Delete

589477

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/873,881A TIME: 15:47:16

Input Set : A:\corrected sequence listing for Scott et al

DATE: 10/15/2001

Output Set: N:\CRF3\10152001\1873881A.raw

```
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:912 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:989 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:993 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:997 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1001 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1995 SEQ:19
L:1117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
L:1117 M:112 C: (48) String data converted to lower case,
L:1117 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1979 Found:1995 SEQ:19
```